



Part of #14/B

SEQUENCE LISTING

<110> Miller, Brian S.
Shetty, Jayarama K.

<120> Modified Forms of Pullulanase

<130> GC396-2

<140> 09/262,126
<141> 1999-03-03

<160> 9 ✓

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 2794
<212> DNA
<213> Bacillus deramificans

<220>
<221> misc_feature
<222> (1)...(2794)
<223> n = A, T, C, or G

<400> 1

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gctgacttt	ttggagctgt	tgcaagtgt	gatattccag	gaaacccaag	tcaggttagga	180
attatcgttc	gcactcaaga	ttggaccaa	gatgtgagcg	ctgaccgcta	catagattta	240
agcaaaggaa	atgaggtgt	gcttgtagaa	ggaaacagcc	aaatttttta	taataaaaaa	300
gatgctgagg	atgcagctaa	acccgctgt	agcaacgctt	attnagatgc	ttcaaacccag	360
gtgctggta	aacttagcca	gccgttaact	cttgggaag	gnnnaagcgg	ctttacggtt	420
catgacgaca	cagcaaataa	ggatattca	gtgacatctg	tgaaggatgc	aagtcttggt	480
caagatgtaa	ccgctgtttt	ggcaggtacc	ttccaacata	tttttgagg	ttccgattgg	540
gcacctgata	atcacagtac	tttattaaaa	aaggtgacta	acaatctcta	tcaattctca	600
ggagatcttc	ctgaaggaaa	ctaccaatat	aaagtggctt	taaatgatag	ctggaataat	660
ccgagttacc	catctgacaa	cattaattta	acagtcctg	ccggcggtgc	acacgtca	720
ttttcgtata	ttccgtccac	tcatgcagtc	tatgacacaa	ttaataatcc	taatcgggat	780
ttacaagttag	aaagcgggt	taaaacggat	ctcgtgacgg	ttactcttagg	ggaagatcca	840
gatgtgagcc	atactctgtc	cattcaaaaca	gatggctatc	aggcaagca	ggtgatacc	900
cgtaatgtgc	ttaattcatac	acagtactac	tattcaggag	atgatcttgg	gaataccat	960
acacagaaaag	caacaacctt	taaagtctgg	gcaccaactt	ctactcaagt	aaatgttctt	1020
ctttatgaca	gtgcaacggg	ttctgtaaaca	aaaatcgatc	ctatgacggc	atcgggcccatt	1080
ggtgtgtggg	aagcaacggt	taatcaaaac	cttggaaaatt	ggtattacat	gtatgaggt	1140
acaggccaaag	gctctacccg	aacggctgtt	gatcctttag	caactgcgt	tgcaccaat	1200
gaaacgagag	gcatgattgt	ggacctggct	aaaacagatc	ctgctggctg	gaacagtgt	1260
aaacatatttca	cgcacaaagaa	tatagaagat	gaggctatct	atgaaatgga	tgtccgtgac	1320
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aaaggaacaa	agggccctga	caacgtaaag	acggggatag	attccttaaa	acaacttggg	1440
attactcatg	ttcagcttat	gcctgttttc	gcatctaaca	gtgtcgatga	aactgatcca	1500
acccaagata	attggggat	tgaccctcg	aactatgtat	ttcctgaagg	gcagtatgt	1560
acaaatgcgt	atggtaatgc	tcgtataaaa	gagtttaagg	aaatggttct	ttcactccat	1620
cgtgaacaca	ttggggat	catggatgtt	gtctataatc	ataccttgc	cacgcaatc	1680
tctgacttcg	ataaaattgt	accagaatat	tattaccgt	cgatgatcca	ggtattata	1740

ccaacggatc	aggtaactgga	aatgaaattt	cangcngaaa	ggccaaatggt	tcaaaaattt	1800
attattgatt	ccctaagta	ttgggtcaat	gagttatcata	ttgacggctt	ccgtttgac	1860
ttaatggcgc	tgctggaaa	agacacgatg	tccaaagctg	cctcgagct	tcatgttatt	1920
aatccagggaa	ttgacttta	cggtagcca	tggacgggtg	gaaccttcgc	actgccagat	1980
gatcagcttc	tgacaaaagg	agctcaaaaa	ggcatggag	tagcggtt	taatgacaat	2040
ttacgaaacg	cgttggacgg	caatgtctt	gattttccg	ctcaagggtt	tgcgacagg	2100
gcaacaggt	taactgtgc	aattaagaat	ggcgttgagg	ggagtattaa	tgactttacc	2160
tcttcaccag	gtgagacaat	taactatgtc	acaagtcatg	ataactacac	ccttgggac	2220
aaaatagccc	taagaatcc	taatgattcc	gaagcggatc	ggattaaaat	ggatgaactc	2280
gcacaaggcag	ttgttatgac	ctcacaaggc	gttccattca	tgcaaggcgg	gaaagaaaatg	2340
cttcgtanaa	aaggcggcaa	cgacaatagt	tataatgcag	gcgatgcggt	caatgagttt	2400
gattggagca	gaaaagctca	atatccagat	gtttcaact	attatacggt	gctaatccac	2460
cttcgtcttg	atcacccagc	cttccgcatg	acgacagct	atgaaatcaa	tagccacctc	2520
caattcctaa	atagtccaga	gaacacagt	gcctatgaat	taactgtca	tgttaataaa	2580
gacaaatggg	gaaatatcat	tgttgtttat	aacccaaata	aaactgttagc	aaccatcaat	2640
ttgccgagcg	gaaaatggc	aatcaatgt	acgagcggta	agtagagaga	atccaccctt	2700
ggtcaagcag	agggaaagtgt	ccaaagtacca	ggtatatact	tgtatgtcct	tcatcaagag	2760
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<210> 2
<211> 956
<212> PRT
<213> *Bacillus deramificans*

<220>
<221> VARIANT
<222> (1)...(956)
<223> Xaa = Any Amino Acid

<400> 2

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					20				25				30		
Thr	Thr	Thr	Ile	Ile	Val	His	Tyr	Phe	Cys	Pro	Ala	Gly	Asp	Tyr	Gln
					35			40				45			
Pro	Trp	Ser	Leu	Trp	Met	Trp	Pro	Lys	Asp	Gly	Gly	Gly	Ala	Glu	Tyr
					50			55			60				
Asp	Phe	Asn	Gln	Pro	Ala	Asp	Ser	Phe	Gly	Ala	Val	Ala	Ser	Ala	Asp
					65			70			75		80		
Ile	Pro	Gly	Asn	Pro	Ser	Gln	Val	Gly	Ile	Ile	Val	Arg	Thr	Gln	Asp
					85			90				95			
Trp	Thr	Lys	Asp	Val	Ser	Ala	Asp	Arg	Tyr	Ile	Asp	Leu	Ser	Lys	Gly
					100			105			110				
Asn	Glu	Val	Trp	Leu	Val	Glu	Gly	Asn	Ser	Gln	Ile	Phe	Tyr	Asn	Glu
					115			120			125				
Lys	Asp	Ala	Glu	Asp	Ala	Ala	Lys	Pro	Ala	Val	Ser	Asn	Ala	Tyr	Leu
					130			135			140				
Asp	Ala	Ser	Asn	Gln	Val	Leu	Val	Lys	Leu	Ser	Gln	Pro	Leu	Thr	Leu
					145			150			155		160		
Gly	Glu	Gly	Xaa	Ser	Gly	Phe	Thr	Val	His	Asp	Asp	Thr	Ala	Asn	Lys
					165			170			175				
Asp	Ile	Pro	Val	Thr	Ser	Val	Lys	Asp	Ala	Ser	Leu	Gly	Gln	Asp	Val
					180			185			190				
Thr	Ala	Val	Leu	Ala	Gly	Thr	Phe	Gln	His	Ile	Phe	Gly	Gly	Ser	Asp
					195			200			205				
Trp	Ala	Pro	Asp	Asn	His	Ser	Thr	Leu	Leu	Lys	Val	Thr	Asn	Asn	

210	215	220													
Leu	Tyr	Gln	Phe	Ser	Gly	Asp	Leu	Pro	Glu	Gly	Asn	Tyr	Gln	Tyr	Lys
225					230				235						240
Val	Ala	Leu	Asn	Asp	Ser	Trp	Asn	Asn	Ser	Tyr	Pro	Ser	Asp	Asn	Ile
					245				250						255
Asn	Leu	Thr	Val	Pro	Ala	Gly	Gly	Ala	His	Val	Thr	Phe	Ser	Tyr	Ile
					260				265						270
Pro	Ser	Thr	His	Ala	Val	Tyr	Asp	Thr	Ile	Asn	Asn	Pro	Asn	Ala	Asp
					275				280						285
Leu	Gln	Val	Glu	Ser	Gly	Val	Lys	Thr	Asp	Leu	Val	Thr	Val	Thr	Leu
					290				295						300
Gly	Glu	Asp	Pro	Asp	Val	Ser	His	Thr	Leu	Ser	Ile	Gln	Thr	Asp	Gly
					305				310			315			320
Tyr	Gln	Ala	Lys	Gln	Val	Ile	Pro	Arg	Asn	Val	Leu	Asn	Ser	Ser	Gln
					325				330						335
Tyr	Tyr	Tyr	Ser	Gly	Asp	Asp	Leu	Gly	Asn	Thr	Tyr	Thr	Gln	Lys	Ala
					340				345						350
Thr	Thr	Phe	Lys	Val	Trp	Ala	Pro	Thr	Ser	Thr	Gln	Val	Asn	Val	Leu
					355				360						365
Leu	Tyr	Asp	Ser	Ala	Thr	Gly	Ser	Val	Thr	Lys	Ile	Val	Pro	Met	Thr
					370				375						380
Ala	Ser	Gly	His	Gly	Val	Trp	Glu	Ala	Thr	Val	Asn	Gln	Asn	Leu	Glu
					385				390			395			400
Asn	Trp	Tyr	Tyr	Met	Tyr	Glu	Val	Thr	Gly	Gln	Gly	Ser	Thr	Arg	Thr
					405				410						415
Ala	Val	Asp	Pro	Tyr	Ala	Thr	Ile	Ala	Pro	Asn	Gly	Thr	Arg	Gly	
					420				425						430
Met	Ile	Val	Asp	Leu	Ala	Lys	Thr	Asp	Pro	Ala	Gly	Trp	Asn	Ser	Asp
					435				440						445
Lys	His	Ile	Thr	Pro	Lys	Asn	Ile	Glu	Asp	Glu	Val	Ile	Tyr	Glu	Met
					450				455						460
Asp	Val	Arg	Asp	Phe	Ser	Ile	Asp	Pro	Asn	Ser	Gly	Met	Lys	Asn	Lys
					465				470			475			480
Gly	Lys	Tyr	Leu	Ala	Leu	Thr	Glu	Lys	Gly	Thr	Lys	Gly	Pro	Asp	Asn
					485				490						495
Val	Lys	Thr	Gly	Ile	Asp	Ser	Leu	Lys	Gln	Leu	Gly	Ile	Thr	His	Val
					500				505						510
Gln	Leu	Met	Pro	Val	Phe	Ala	Ser	Asn	Ser	Val	Asp	Glu	Thr	Asp	Pro
					515				520						525
Thr	Gln	Asp	Asn	Trp	Gly	Tyr	Asp	Pro	Arg	Asn	Tyr	Asp	Val	Pro	Glu
					530				535						540
Gly	Gln	Tyr	Ala	Thr	Asn	Ala	Asn	Gly	Asn	Ala	Arg	Ile	Lys	Glu	Phe
					545				550			555			560
Lys	Glu	Met	Val	Leu	Ser	Leu	His	Arg	Glu	His	Ile	Gly	Val	Asn	Met
					565				570						575
Asp	Val	Val	Tyr	Asn	His	Thr	Phe	Ala	Thr	Gln	Ile	Ser	Asp	Phe	Asp
					580				585						590
Lys	Ile	Val	Pro	Glu	Tyr	Tyr	Arg	Thr	Met	Ile	Gln	Val	Ile	Ile	
					595				600						605
Pro	Thr	Asp	Gln	Val	Leu	Glu	Met	Lys	Leu	Xaa	Ala	Glu	Arg	Pro	Met
					610				615						620
Val	Gln	Lys	Phe	Ile	Ile	Asp	Ser	Leu	Lys	Tyr	Trp	Val	Asn	Glu	Tyr
					625				630			635			640
His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Leu	Met	Ala	Leu	Leu	Gly	Lys	Asp
					645				650						655
Thr	Met	Ser	Lys	Ala	Ala	Ser	Glu	Leu	His	Ala	Ile	Asn	Pro	Gly	Ile
					660				665						670

Ala Leu Tyr Gly Glu Pro Trp Thr Gly Gly Thr Ser Ala Leu Pro Asp
 675 680 685
 Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met Gly Val Ala Val
 690 695 700
 Phe Asn Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn Val Phe Asp Ser
 705 710 715 720
 Ser Ala Gln Gly Phe Ala Thr Gly Ala Thr Gly Leu Thr Asp Ala Ile
 725 730 735
 Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr Ser Ser Pro Gly
 740 745 750
 Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp
 755 760 765
 Lys Ile Ala Leu Ser Asn Pro Asn Asp Ser Glu Ala Asp Arg Ile Lys
 770 775 780
 Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser Gln Gly Val Pro
 785 790 795 800
 Phe Met Gln Gly Gly Glu Glu Met Leu Arg Xaa Lys Gly Gly Asn Asp
 805 810 815
 Asn Ser Tyr Asn Ala Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg
 820 825 830
 Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly Leu Ile His
 835 840 845
 Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile
 850 855 860
 Asn Ser His Leu Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr
 865 870 875 880
 Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp Gly Asn Ile Ile Val
 885 890 895
 Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly
 900 905 910
 Lys Trp Ala Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu
 915 920 925
 Gly Gln Ala Glu Gly Ser Val Gln Val Pro Gly Ile Ser Met Met Ile
 930 935 940
 Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys
 945 950 955

<210> 3
 <211> 718
 <212> PRT
 <213> Bacillus subtilis

<400> 3

Met	Val	Ser	Ile	Arg	Arg	Ser	Phe	Glu	Ala	Tyr	Val	Asp	Asp	Met	Asn
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														30	
Pro	Phe	Arg	Leu	Glu	Thr	Glu	Ile	Thr	Asp	Phe	Pro	Leu	Ala	Val	Arg
														45	
Glu	Glu	Tyr	Ser	Leu	Glu	Ala	Lys	Tyr	Lys	Tyr	Val	Cys	Val	Ser	Asp
														50	
His	Pro	Val	Thr	Phe	Gly	Lys	Ile	His	Cys	Val	Arg	Ala	Ser	Ser	Gly
														65	
His	Lys	Thr	Asp	Leu	Gln	Ile	Gly	Ala	Val	Ile	Arg	Thr	Ala	Ala	Phe
														85	
Asp	Asp	Glu	Phe	Tyr	Tyr	Asp	Gly	Glu	Leu	Gly	Ala	Val	Tyr	Thr	Ala
														100	
														105	
														110	

Asp His Thr Val Phe Lys Val Trp Ala Pro Ala Ala Thr Ser Ala Ala
 115 120 125
 Val Lys Leu Ser His Pro Asn Lys Ser Gly Arg Thr Phe Gln Met Thr
 130 135 140
 Arg Leu Glu Lys Gly Val Tyr Ala Val Thr Val Thr Gly Asp Leu His
 145 150 155 160
 Gly Tyr Glu Tyr Leu Phe Cys Ile Cys Asn Asn Ser Glu Trp Met Glu
 165 170 175
 Thr Val Asp Gln Tyr Ala Lys Ala Val Thr Val Asn Gly Glu Lys Gly
 180 185 190
 Val Val Leu Arg Pro Asp Gln Met Lys Trp Thr Ala Pro Leu Lys Pro
 195 200 205
 Phe Ser His Pro Val Asp Ala Val Ile Tyr Glu Thr His Leu Arg Asp
 210 215 220
 Phe Ser Ile His Glu Asn Ser Gly Met Ile Asn Lys Gly Lys Tyr Leu
 225 230 235 240
 Ala Leu Thr Glu Thr Asp Thr Gln Thr Ala Asn Gly Ser Ser Gly
 245 250 255
 Leu Ala Tyr Val Lys Glu Leu Gly Val Thr His Val Glu Leu Leu Pro
 260 265 270
 Val Asn Asp Phe Ala Gly Val Asp Glu Glu Lys Pro Leu Asp Ala Tyr
 275 280 285
 Asn Trp Gly Tyr Asn Pro Leu His Phe Phe Ala Pro Glu Gly Ser Tyr
 290 295 300
 Ala Ser Asn Pro His Asp Pro Gln Thr Arg Lys Thr Glu Leu Lys Gln
 305 310 315 320
 Met Ile Asn Thr Leu His Gln His Gly Leu Arg Val Ile Leu Asp Val
 325 330 335
 Val Phe Asn His Val Tyr Lys Arg Glu Asn Ser Pro Phe Glu Lys Thr
 340 345 350
 Val Pro Gly Tyr Phe Phe Arg His Asp Glu Cys Gly Met Pro Ser Asn
 355 360 365
 Gly Thr Gly Val Gly Asn Asp Ile Ala Ser Glu Arg Arg Met Ala Arg
 370 375 380
 Lys Phe Ile Ala Asp Cys Val Val Tyr Trp Leu Glu Glu Tyr Asn Val
 385 390 395 400
 Asp Gly Phe Arg Phe Asp Leu Leu Gly Ile Leu Asp Ile Asp Thr Val
 405 410 415
 Leu Tyr Met Lys Glu Lys Ala Thr Lys Ala Lys Pro Gly Ile Leu Leu
 420 425 430
 Phe Gly Glu Gly Trp Asp Leu Ala Thr Pro Leu Pro His Glu Gln Lys
 435 440 445
 Ala Ala Leu Ala Asn Ala Pro Arg Met Pro Gly Ile Gly Phe Phe Asn
 450 455 460
 Asp Met Phe Arg Asp Ala Val Lys Gly Asn Thr Phe His Leu Lys Ala
 465 470 475 480
 Thr Gly Phe Ala Leu Gly Asn Gly Glu Ser Ala Gln Ala Val Met His
 485 490 495
 Gly Ile Ala Gly Ser Ser Gly Trp Lys Ala Leu Ala Pro Ile Val Pro
 500 505 510
 Glu Pro Ser Gln Ser Ile Asn Tyr Val Glu Ser His Asp Asn His Thr
 515 520 525
 Phe Trp Asp Lys Met Ser Phe Ala Leu Pro Gln Glu Asn Asp Ser Arg
 530 535 540
 Lys Arg Ser Arg Gln Arg Leu Ala Val Ala Ile Ile Leu Leu Ala Gln
 545 550 555 560
 Gly Val Pro Phe Ile His Ser Gly Gln Glu Phe Phe Arg Thr Lys Gln

	565	570	575
Gly Val Glu Asn Ser Tyr Gln Ser Ser Asp Ser Ile Asn Gln Leu Asp			
580	585	590	
Trp Asp Arg Arg Glu Thr Phe Lys Glu Asp Val His Tyr Ile Arg Arg			
595	600	605	
Leu Ile Ser Leu Arg Lys Ala His Pro Ala Phe Arg Leu Arg Ser Ala			
610	615	620	
Ala Asp Ile Gln Arg His Leu Glu Cys Leu Thr Leu Lys Glu His Leu			
625	630	635	640
Ile Ala Tyr Arg Leu Tyr Asp Leu Asp Glu Val Asp Glu Trp Lys Asp			
645	650	655	
Ile Ile Val Ile His His Ala Ser Pro Asp Ser Val Glu Trp Arg Leu			
660	665	670	
Pro Asn Asp Ile Pro Tyr Arg Leu Leu Cys Asp Pro Ser Gly Phe Gln			
675	680	685	
Glu Asp Pro Thr Glu Ile Lys Lys Thr Val Ala Val Asn Gly Ile Gly			
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Thr Val Ile Leu Tyr Leu Ala Ser Asp Leu Lys Ser Phe Ala			
705	710	715	

<210> 4

<211> 1091

<212> PRT

<213> Klebsiella pneumonia

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Pro Asp Thr Pro Asp Asn Gln Asp Val Val Val Arg Leu Pro Asp Val			
35	40	45	
Ala Val Pro Gly Glu Ala Val Thr Ala Val Glu Asn Gln Ala Val Ile			
50	55	60	
His Leu Val Asp Ile Ala Gly Ile Thr Ser Ser Ala Ala Asp Tyr			
65	70	75	80
Ser Ser Lys Asn Leu Tyr Leu Trp Asn Asn Glu Thr Cys Asp Ala Leu			
85	90	95	
Ser Ala Pro Val Ala Asp Trp Asn Asp Val Ser Thr Thr Pro Ser Gly			
100	105	110	
Ser Asp Lys Tyr Gly Pro Tyr Trp Val Ile Pro Leu Asn Lys Glu Ser			
115	120	125	
Gly Cys Ile Asn Val Ile Val Arg Asp Gly Thr Asp Lys Leu Ile Asp			
130	135	140	
Ser Asp Leu Arg Val Ala Phe Gly Asp Phe Thr Asp Arg Thr Val Ser			
145	150	155	160
Val Ile Ala Gly Asn Ser Ala Val Tyr Asp Ser Arg Ala Asp Ala Phe			
165	170	175	
Arg Ala Ala Phe Gly Val Ala Leu Ala Glu Ala His Trp Val Asp Lys			
180	185	190	
Asn Thr Leu Leu Trp Pro Gly Gly Gln Asp Lys Pro Ile Val Arg Leu			
195	200	205	
Tyr Tyr Ser His Ser Ser Lys Val Ala Ala Asp Gly Glu Gly Lys Phe			
210	215	220	
Thr Asp Arg Tyr Leu Lys Leu Thr Pro Thr Thr Val Ser Gln Gln Val			
225	230	235	240
Ser Met Arg Phe Pro His Leu Ser Ser Tyr Ala Ala Phe Lys Leu Pro			

245	250	255
Asp Asn Ala Asn Val Asp Glu Leu Leu Gln Gly Glu Thr Val Ala Ile		
260	265	270
Ala Ala Ala Glu Asp Gly Ile Leu Ile Ser Ala Thr Gln Val Gln Thr		
275	280	285
Ala Gly Val Leu Asp Asp Ala Tyr Ala Glu Ala Ala Glu Ala Leu Ser		
290	295	300
Tyr Gly Ala Gln Leu Ala Asp Gly Gly Val Thr Phe Arg Val Trp Ala		
305	310	315
Pro Thr Ala Gln Gln Val Asp Val Val Val Tyr Ser Ala Asp Lys Lys		
325	330	335
Val Ile Gly Ser His Pro Met Thr Arg Asp Ser Ala Ser Gly Ala Trp		
340	345	350
Ser Trp Gln Gly Gly Ser Asp Leu Lys Gly Ala Phe Tyr Arg Tyr Ala		
355	360	365
Met Thr Val Tyr His Pro Gln Ser Arg Lys Val Glu Gln Tyr Glu Val		
370	375	380
Thr Asp Pro Tyr Ala His Ser Leu Ser Thr Asn Ser Glu Tyr Ser Gln		
385	390	395
Val Val Asp Leu Asn Asp Ser Ala Leu Lys Pro Asp Gly Trp Asp Asn		
405	410	415
Leu Thr Met Pro His Ala Gln Lys Thr Lys Ala Asp Leu Ala Lys Met		
420	425	430
Thr Ile His Glu Ser His Ile Arg Asp Leu Ser Ala Trp Asp Gln Thr		
435	440	445
Val Pro Ala Glu Leu Arg Gly Lys Tyr Leu Ala Leu Thr Ala Gly Asp		
450	455	460
Ser Asn Met Val Gln His Leu Lys Thr Leu Ser Ala Ser Gly Val Thr		
465	470	475
His Val Glu Leu Leu Pro Val Phe Asp Leu Ala Thr Val Asn Glu Phe		
485	490	495
Ser Asp Lys Val Ala Asp Ile Gln Gln Pro Phe Ser Arg Leu Cys Glu		
500	505	510
Val Asn Ser Ala Val Lys Ser Ser Glu Phe Ala Gly Tyr Cys Asp Ser		
515	520	525
Gly Ser Thr Val Glu Glu Val Leu Asn Gln Leu Lys Gln Ser Asp Ser		
530	535	540
Gln Asp Asn Pro Gln Val Gln Ala Leu Asn Thr Leu Val Ala Gln Thr		
545	550	555
Asp Ser Tyr Asn Trp Gly Tyr Asp Pro Phe His Tyr Thr Val Pro Glu		
565	570	575
Gly Ser Tyr Ala Thr Asp Pro Glu Gly Thr Thr Arg Ile Lys Glu Phe		
580	585	590
Arg Thr Met Ile Gln Ala Ile Lys Gln Asp Leu Gly Met Asn Val Ile		
595	600	605
Met Asp Val Val Tyr Asn His Thr Asn Ala Ala Gly Pro Thr Asp Arg		
610	615	620
Thr Ser Val Leu Asp Lys Ile Val Pro Trp Tyr Tyr Gln Arg Leu Asn		
625	630	635
Glu Thr Thr Gly Ser Val Glu Ser Ala Thr Cys Cys Ser Asp Ser Ala		
645	650	655
Pro Glu His Arg Met Phe Ala Lys Leu Ile Ala Asp Ser Leu Ala Val		
660	665	670
Trp Thr Thr Asp Tyr Lys Ile Asp Gly Phe Arg Phe Asp Leu Met Gly		
675	680	685
Tyr His Pro Lys Ala Gln Ile Leu Ser Ala Trp Glu Arg Ile Lys Ala		
690	695	700

Leu Asn Pro Asp Ile Tyr Phe Phe Gly Glu Gly Trp Asp Ser Asn Gln
 705 710 715 720
 Ser Asp Arg Phe Glu Ile Ala Ser Gln Ile Asn Leu Lys Gly Thr Gly
 725 730 735
 Ile Gly Thr Phe Ser Asp Arg Leu Arg Asp Ser Val Arg Gly Gly Gly
 740 745 750
 Pro Phe Asp Ser Gly Asp Ala Leu Arg Gln Asn Gln Gly Ile Gly Ser
 755 760 765
 Gly Ala Gly Val Leu Pro Asn Glu Leu Ala Ser Leu Ser Asp Asp Gln
 770 775 780
 Val Arg His Leu Ala Asp Leu Thr Arg Leu Gly Met Ala Gly Asn Leu
 785 790 795 800
 Ala Asp Phe Val Met Ile Asp Lys Asp Gly Ala Ala Lys Lys Gly Ser
 805 810 815
 Glu Ile Asp Tyr Asn Gly Ala Pro Gly Gly Tyr Ala Ala Asp Pro Thr
 820 825 830
 Glu Val Val Asn Tyr Val Ser Lys His Asp Asn Gln Thr Leu Trp Asp
 835 840 845
 Met Ile Ser Tyr Lys Ala Ser Gln Glu Ala Asp Leu Ala Thr Arg Val
 850 855 860
 Arg Met Gln Ala Val Ser Leu Ala Thr Val Met Leu Gly Gln Gly Ile
 865 870 875 880
 Ala Phe Asp Gln Gln Gly Ser Glu Leu Leu Arg Ser Lys Ser Phe Thr
 885 890 895
 Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Arg Val Asp Tyr Ser
 900 905 910
 Leu Gln Asp Asn Asn Tyr Asn Val Gly Met Pro Arg Ile Ser Asp Asp
 915 920 925
 Gly Ser Asn Tyr Glu Val Ile Thr Arg Val Lys Glu Met Val Ala Thr
 930 935 940
 Pro Gly Glu Ala Glu Leu Lys Gln Met Thr Ala Phe Tyr Gln Glu Leu
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